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Molecular epidemiology and genetic diversity of geminiviruses in sub-Saharan Africa and the south-west Indian Ocean islands

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Molecular epidemiology, genetic diversity and dissemination routes of CMGs in sub-Saharan Africa and the south-west Indian Ocean (SWIO) islands

Cassava cultivation is associated with a wide range of diseases that seriously undermine the food and economic security in African countries. The most notable of these is CMD, caused by a complex of cassava mosaic geminiviruses (CMGs; *Geminiviridae*, *Begomovirus*). To better understand the epidemiology of CMD as a major constraint of cassava production, we investigated a large-scale plant epidemiological survey in Central African Republic (CAR) and Madagascar, as part of two PhDs with a CAR student, Innocent Zinga (2010-2012), and a Malagasy student, Mireille Harimalala (2010-2012). CMD was shown to be the most serious constraint to cassava in both countries (Harimalala et al., 2014; Zinga et al., 2013). CMD is distributed throughout the two countries, with an average incidence of 85% in CAR. Importantly, 94% and 95% of diseased plants collected in CAR and Madagascar, respectively, had cutting-derived CMD infection, suggesting that farmers mostly use virus-infected cuttings for planting. Molecular diagnosis revealed that the causal agents of CMD in CAR, Chad (Zinga et al., 2012), and Burkina Faso (Tiendrébéogo et al., 2009) are ACMV and/or EACMV-UG. We also demonstrated that 58% of CMD samples of CAR present mixed infections (ACMV and EACMV-UG) and that the severity of symptoms was significantly higher in these samples (Zinga et al., 2013). Molecular diagnosis of CMGs in Madagascar revealed an unprecedented diversity of six species: ACMV, EACMCV, EACMKV, EACMV, SACMV, and CMMGV (Harimalala et al., 2014; Harimalala et al., 2012). Distinct geographical distributions were observed for the six species in Madagascar. While ACMV was more prevalent in the central highlands, EACMV and EACMKV were prevalent in lowlands and coastal regions. Molecular diagnosis revealed that mixed infection (up to four co-infected viruses) occurred in 21% of the samples and was associated with higher symptom severity scores. All our results suggest that mixed infection and synergism between CMGs could be an important feature in the low yields of cassava plants in these countries, similar to the severe CMD epidemics reported in East Africa. Given the sampling locations, sampling dates, and full genome sequences of hundreds of CMG isolates sampled during 1996–2009, we statistically retraced the historical migration routes of these viruses across sub-Saharan Africa and the SWIO islands (De Bruyn et al., 2012). Phylogeographic analyses suggest that presence of CMGs on these islands is likely the result of their being introduced at least four times independently from mainland Africa between 1988 and 2009. Our results suggest that anthropic factors may play a major role in the spread of CMGs, as the principal axes of viral migration correspond with major routes of human movement and commercial trade.

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